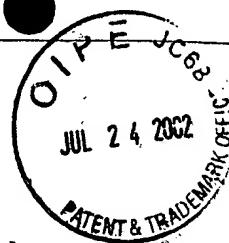


SEQUENCE LISTING



RECEIVED

JUL 31 2002

TECH CENTER 1600/2900

<110> Emil D. Kakkis
Becky Tanamachi

<120> Recombinant Alpha-L-Iduronidase, Methods
for Producing and Purifying the Same and Methods for
Treating Diseases Caused by Deficiencies Thereof

<130> 08000051US00

<140> 09/439,923
<141> 1999-11-12

<160> 2 ✓

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 6200
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1558)...(3516)

<400> 1

gacggatcg gagatctccc gatcccstat ggtcgactct cagtacaatc tgctctgatg 60
 ccgcatagtt aagccagtt ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg 120
 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatt aagaatctgc 180
 ttagggtag gcgtttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240
 gattatttgc tagttattaa tagtaatcaa ttacggggtc attagttcat agccatata 300
 tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 360
 cccgcccatt gacgtcaata atgacgtatg ttccatagt aacgccaata gggactttcc 420
 attgacgtca atgggtggac tatttacggt aaactgccc cttggcagta catcaagtgt 480
 atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540
 atgcccagta catgaccta tgggacttgc ctacttggca gtacatctac gtattagtca 600
 tcgctattac catggtgatg cggtttggc agtacatcaa tggcgtgga tagcggtttg 660
 actcacgggg atttccaagt ctccacccca ttgacgtcaa tggaggtttg tttggcacc 720
 aaaatcaacg ggactttcca aatgtcgta acaactccgc cccattgacg caaatggcg 780
 gttaggcgtgt acgggtggag gtctatataa gcagagctct ctggcttaact agagaaccca 840
 ctgcttaact ggcttatcg aattaatacg actcactata gggagaccca agttcgcag 900
 aattcctgcg gctgctacag tgggtccagc gtctgcctg gctgtgtga gctgtggAAC 960
 agtggcgcat cattcaagtg cacagttacc catcctgagt ctggcacctt aactggcaca 1020
 attgccaaag tcacaggtga gtcagatgc ataccaggac attgtatgac gttccctgct 1080
 cacatgcctg ctttcttcct ataatacaga tggtaacta actgctcatg tccttatatc 1140
 acagagggaa attggagcta tctgaggaac tgcccagaag ggaagggcag aggggtctt 1200
 ctctccttgt ctgagccata actcttctt ctaccccttca gtgaacaccc tcccacccca 1260
 ggtccacctg ctaccgcgc cgtcggagga gctggccctg aatgagctct tggccctgac 1320
 atgcctgggt cgagtttca accctaaaga agtgcgtgt cgatggctgc atggaaatga 1380
 ggagctgtcc ccagaaagct acctagtgtt tgagccctta aaggagccag gctggggagc 1440
 caccacccatc ctggtgacaa gctgtgtgc tggatcgat gaaagttga tattcaattc 1500
 cggaggcgga accggcagtg cagcccaag cccgcagtc cccgagcacg cgtggcc atg 1560

Met

1

cgt ccc ctg cgc ccc cgcc gctg ctg gcg ctc ctg gcc tgg ctc
Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Ala Ser Leu 1608

ctg gcc gcc ccc ccg gtg gcc ccg gag gcc ccg cac ctg gtg cat Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val His 20	25	30	1656
gtg gac gcg gcc cgc gcg ctg tgg ccc ctg cgg cgc ttc tgg agg agc Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser 35	40	45	1704
aca ggc ttc tgc ccc ccg ctg cca cac agc cag gct gac cag tac gtc Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr Val 50	55	60	1752
ctc agc tgg gac cag cag ctc aac ctc gcc tat gtg ggc gcc gtc cct Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val Pro 70	75	80	1800
cac cgc ggc atc aag cag gtc cgg acc cac tgg ctg ctg gag ctt gtc His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu Val 85	90	95	1848
acc acc agg ggg tcc act gga cgg ggc ctg agc tac aac ttc acc cac Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr His 100	105	110	1896
ctg gac ggg tac ctg gac ctt ctc agg gag aac cag ctc ctc cca ggg Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro Gly 115	120	125	1944
ttt gag ctg atg ggc agc gcc tcg ggc cac ttc act gac ttt gag gac Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu Asp 130	135	140	1992
aag cag cag gtg ttt gag tgg aag gac ttg gtc tcc agc ctg gcc agg Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala Arg 150	155	160	2040
aga tac atc ggt agg tac gga ctg gcg cat gtt tcc aag tgg aac ttc Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn Phe 165	170	175	2088
gag acg tgg aat gag cca gac cac cac gac ttt gac aac gtc tcc atg Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser Met 180	185	190	2136
acc atg caa ggc ttc ctg aac tac tac gat gcc tgc tcg gag ggt ctg Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly Leu 195	200	205	2184
cgc gcc gcc agc ccc gcc ctg cgg ctg gga ggc ccc ggc gac tcc ttc Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser Phe 210	215	220	2232
cac agg cca ccg cga tcc ccg ctg agc tgg ggc ctc ctg cgc cac tgc His Arg Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His Cys 230	235	240	2280
cac gac ggt acc aac ttc ttc act ggg gag gcg ggc gtg cgg ctg gac His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu Asp 245	250	255	2328

tac atc tcc ctc cac agg aag ggt gcg cgc agc tcc atc tcc atc ctg Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile Leu 260 265 270	2376
gag cag gag aag gtc gtc gcg cag cag atc cgg cag ctc ttc ccc aag Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro Lys 275 280 285	2424
ttc gcg gac acc ccc att tac aac gac gag gcg gac ccc ctg gtg ggc Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val Gly 290 295 300 305	2472
tgg tcc ctg cca cag ccg tgg agg gcg gac gtg acc tac gcg gcc atg Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala Met 310 315 320	2520
gtg gtg aag gtc atc gcg cag cat cag aac ctg cta ctg gcc aac acc Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr 325 330 335	2568
acc tcc gcc ttc ccc tac gcg ctc ctg agc aac gac aat gcc ttc ctg Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu 340 345 350	2616
agc tac cac ccg cac ccc ttc gcg cag cgc acg ctc acc gcg cgc ttc Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe 355 360 365	2664
cag gtc aac aac acc cgc ccg cac gtg cag ctg ttg cgc aag ccg Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys Pro 370 375 380 385	2712
gtg ctc acg gcc atg ggg ctg ctg gcg ctg ctg gat gag gag cag ctc Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln Leu 390 395 400	2760
tgg gcc gaa gtg tcg cag gcc ggg acc gtc ctg gac agc aac cac acg Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His Thr 405 410 415	2808
gtg ggc gtc ctg gcc agc gcc cac cgc ccc cag ggc ccg gcc gac gcc Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp Ala 420 425 430	2856
tgg cgc gcc gcg gtg ctg atc tac gcg agc gac gac acc cgc gcc cac Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His 435 440 445	2904
ccc aac cgc agc gtc gcg gtg acc ctg cgg ctg cgc ggg gtg ccc ccc Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro 450 455 460 465	2952
ggc ccg ggc ctg gtc tac gtc acg cgc tac ctg gac aac ggg ctc tgc Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys 470 475 480	3000
agc ccc gac ggc gag tgg cgg cgc ctg ggc cgg ccc gtc ttc ccc acg Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro Thr 485 490 495	3048

gca gag cag ttc cgg cgc atg cgc gcg gct gag gac ccg gtg gcc gcg 3096
 Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala Ala
 500 505 510

gcg ccc cgc ccc tta ccc gcc ggc ggc cgc ctg acg ctg cgc ccc gcg 3144
 Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro Ala
 515 520 525

ctg cgg ctg ccc tcg ctt ttg ctg gtg cac gtg tgt gcg cgc ccc gag 3192
 Leu Arg Leu Pro Ser Leu Leu Val His Val Cys Ala Arg Pro Glu
 530 535 540 545

aag ccg ccc ggg cag gtc acg cgg ctc cgc gcc ctg ccc ctg acc caa 3240
 Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln
 550 555 560

ggg cag ctg gtt ctg gtc tgg tcg gat gaa cac gtg ggc tcc aag tgc 3288
 Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys
 565 570 575

ctg tgg aca tac gag atc cag ttc tct cag gac ggt aag gcg tac acc 3336
 Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr
 580 585 590

ccg gtc agc agg aag cca tcg acc ttc aac ctc ttt gtg ttc agc cca 3384
 Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser Pro
 595 600 605

gac aca ggt gct gtc tct ggc tcc tac cga gtt cga gcc ctg gac tac 3432
 Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp Tyr
 610 615 620 625

tgg gcc cga cca ggc ccc ttc tcg gac cct gtg ccg tac ctg gag gtc 3480
 Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu Val
 630 635 640

cct gtg cca aga ggg ccc cca tcc ccg ggc aat cca tgaggctgtg 3526
 Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
 645 650

ctgagccca gtgggttgc a cttccacccg cagtcagcga gctggggctg cactgtgcc 3586
 atgctgcctt cccatcaccc cctttgcaat atattttat attttaaaaa aaaaaaaaaa 3646
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaagaattcc 3706
 tgcagcccccgg gggatccact agttcttagag ggcccggtta aacccgctga tcagcctcga 3766
 ctgtgccttc tagttgccag ccatcttttgc tttggccctc ccccggtgcct tccttgaccc 3826
 tggaaagggtgc cactccact gtcctttct aataaaatga ggaaatttgc a tgcattgtc 3886
 tgagtaggtg tcattctatt ctgggggtg gggggggca ggacagacaag ggggaggatt 3946
 gggaaagacaa tagcaggcat gctggggatg cggggggctc tatggcttct gaggcggaaa 4006
 gaaccagctg gggctcgaga gcttggcgta atcatggtca tagctgtttc ctgtgtgaaa 4066
 ttgttatccg ctcacaattt cacacaaatc acgagccgaa agcataaaatgtt gtaaaggctg 4126
 ggggtgcctaa tgagttagt aactcacatt aatttgcgtt cgctcacttc cccgtttccaa 4186
 gtcgggaaac ctgtcgtgcc agctgcattt atgaatccggc caacgcgcgg ggagaggcgg 4246
 tttgcgtatt gggcgctt ccgttccctc gctactgac tgcgtgcgtt cggcgttcc 4306
 gctgcggcga gcggtatcag ctcactcaaa ggcggtaata cggttatcca cagaatcagg 4366
 ggataacgca gggaaagaaca tgtgagcaaa agggcagcaa aaggccagga accgtaaaaa 4426
 ggcgcgtt ctggcggtt tccataggct ccgcggccct gacgagcatc acaaaaatcg 4486
 acgctcaagt cagaggtggc gaaacccgac aggactataa agataccagg cgtttcccc 4546
 tggaaagctcc ctggcgctt ctcctgtcc gaccctgccc cttaccggat acctgtccgc 4606
 ctttctccct tcgggaagcg tggcgcttc tcaatgctca cgctgttaggt atctcagttc 4666
 ggtgttaggtc gttcgcttca agctggcgctg tgcacgaa ccccccgttc agcccgaccg 4726
 ctgcgcctta tccggtaact atcgcttgc gtcacccg gtaagacacg acttatcgcc 4786

a
 cont

actggcagca	gccactggta	acaggattag	cagagcgagg	tatgtaggcg	gtgctacaga	4846
gttcttgaag	tggggccta	actacggcta	cactagaagg	acagtatttgc	gtatctgcgc	4906
tctgctgaag	ccagttacct	tcggaaaaag	agttggtagc	tcttgatccg	gcaaacaaac	4966
caccgctgg	agcggtgg	ttttgttg	caagcagcag	attacgcgc	aaaaaaaagg	5026
atctcaagaa	gatccttga	tctttctac	gggtctgac	gctcagtgg	acgaaaactc	5086
acgttaaggg	atttggtca	tgagattatc	aaaaaggatc	ttcacctaga	tccttttaaa	5146
ttaaaaatga	agttttaat	caatctaaag	tatatatgag	taaacttgg	ctgacagtt	5206
ccaatgctta	atcagtgg	cacctatctc	agcgatctgt	ctattcgtt	catccatagt	5266
tgcctgactc	cccgctgtgt	agataactac	gatacgggag	ggcttaccat	ctggccccag	5326
tgctgcaatg	ataccgcgag	acccacgctc	accggctcca	gatttatcag	caataaacc	5386
gccagccgga	aggccgagc	gcagaagtgg	tcctgcaact	ttatccgcct	ccatccagtc	5446
tattaattgt	tgccggaaag	ctagagtaag	tagttcgcca	gttaatagtt	tgcgcaacgt	5506
tgttgcatt	gctacaggca	tcgtgggtc	acgctcg	tttggatgg	cttcattcag	5566
ctccgggtcc	caacgatcaa	ggcgagg	atgatcccc	atgttg	caaaaaacca	5626
tagctcc	ggtcctccg	tcgttgcag	aagtaagtt	gccgcagtgt	tatcactcat	5686
ggttatggca	gcactgcata	attctgtac	tgtcatgcca	tccgtaagat	gctttctgt	5746
gactggtgag	tactcaacca	agtcatctg	agaatagtgt	atgcggcgac	cgagttgctc	5806
ttgcccggcg	tcaatacggg	ataataccgc	gccacatagc	agaactttaa	aagtgc	5866
cattggaaaa	cgttcttcgg	ggcgaaaact	ctcaaggatc	ttaccgctgt	tgagatccag	5926
ttcgatgtaa	cccaactcg	cacccaactg	atcttcagca	tctttactt	tcaccagcgt	5986
ttctgggtga	gaaaaaacag	gaaggcaaaa	tgccgaaaaa	aaggaaataa	gggcgacac	6046
gaaatgtga	atactcatac	tcttc	tcaatattt	tgaagcattt	atcagggtt	6106
ttgtctcatg	agcgatatac	tatttgaatg	tatttagaaa	aataaaacaaa	taggggttcc	6166
gcccacattt	ccccgaaaaag	tgccac	ctga	cg		6200

<210> 2
 <211> 653
 <212> PRT
 <213> Homo sapiens

<400> 2

Met	Arg	Pro	Leu	Arg	Pro	Arg	Ala	Ala	Leu	Leu	Ala	Leu	Ala	Ser	
1			5				10				15				
Leu	Leu	Ala	Ala	Pro	Pro	Val	Ala	Pro	A	Gl	Ala	Pro	His	Leu	Val
						20			25			30			
His	Val	Asp	Ala	Ala	Arg	Ala	Leu	Trp	Pro	Leu	Arg	Arg	Phe	Trp	Arg
						35			40		45				
Ser	Thr	Gly	Phe	Cys	Pro	Pro	Leu	Pro	His	Ser	Gln	Ala	Asp	Gln	Tyr
						50			55		60				
Val	Leu	Ser	Trp	Asp	Gln	Gln	Leu	Asn	Leu	Ala	Tyr	Val	Gly	Ala	Val
						65			70		75		80		
Pro	His	Arg	Gly	Ile	Lys	Gln	Val	Arg	Thr	His	Trp	Leu	Glu	Leu	
						85			90		95				
Val	Thr	Thr	Arg	Gly	Ser	Thr	Gly	Arg	Gly	Leu	Ser	Tyr	Asn	Phe	Thr
						100			105		110				
His	Leu	Asp	Gly	Tyr	Leu	Asp	Leu	Leu	Arg	Glu	Asn	Gln	Leu	Leu	Pro
						115			120		125				
Gly	Phe	Glu	Leu	Met	Gly	Ser	Ala	Ser	Gly	His	Phe	Thr	Asp	Phe	Glu
						130			135		140				
Asp	Lys	Gln	Gln	Val	Phe	Glu	Trp	Lys	Asp	Leu	Val	Ser	Ser	Leu	Ala
						145			150		155		160		
Arg	Arg	Tyr	Ile	Gly	Arg	Tyr	Gly	Leu	Ala	His	Val	Ser	Lys	Trp	Asn
						165			170		175				
Phe	Glu	Thr	Trp	Asn	Glu	Pro	Asp	His	His	Asp	Phe	Asp	Asn	Val	Ser
						180			185		190				
Met	Thr	Met	Gln	Gly	Phe	Leu	Asn	Tyr	Tyr	Asp	Ala	Cys	Ser	Glu	Gly
						195			200		205				
Leu	Arg	Ala	Ala	Ser	Pro	Ala	Leu	Arg	Leu	Gly	Gly	Pro	Gly	Asp	Ser
						210			215		220				
Phe	His	Arg	Pro	Pro	Arg	Ser	Pro	Leu	Ser	Trp	Gly	Leu	Leu	Arg	His
						225			230		235		240		

Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
245 250 255
Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
260 265 270
Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro
275 280 285
Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val
290 295 300
Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala
305 310 315 320
Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn
325 330 335
Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe
340 345 350
Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg
355 360 365
Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys
370 375 380
Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln
385 390 395 400
Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His
405 410 415
Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp
420 425 430
Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala
435 440 445
His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro
450 455 460
Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu
465 470 475 480
Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro
485 490 495
Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala
500 505 510
Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro
515 520 525
Ala Leu Arg Leu Pro Ser Leu Leu Val His Val Cys Ala Arg Pro
530 535 540
Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr
545 550 555 560
Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys
565 570 575
Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr
580 585 590
Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser
595 600 605
Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp
610 615 620
Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
625 630 635 640
Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
645 650